Undecanoic acid.

Conclusion: Methanolic extract of *L. speciosa* flower inhibited the growth of *S. aureus* both *in vitro* and *in vivo*. Significant rescue activity, improved development and no toxicity in *C. elegans* suggests that further investigation to extracts of *L. speciosa* using *C.elegans* will lead to potent anti-infective against drug resistant *S. aureus* infections. {*Supported in part by UGC&DST, GOI funding to KB and LTMT scholarship to SD*}

http://dx.doi.org/10.1016/j.ijid.2012.05.472

Type: Poster Presentation

Final Abstract Number: 54.010
Session: Infection Control, Nosocomial Infections & Critical Care
Date: Saturday, June 16, 2012
Time: 12:45-14:15
Room: Poster & Exhibition Area

Prevalence of bacterial, parasitological and serological infections among food handlers in Kigali Rwanda (2009-2011)

J.B. Gatabazi, J.-F. Flandin*, I. Uwimana, F.G. Niyitegeka, O. Mukabayire

National Reference Laboratory, Kigali, Rwanda

Background: Food handlers represent a possible cause of transmission of infectious diseases. This study was designed to assess the prevalence of intestinal parasites, urinary tract infections and HBV and HIV seroprevalence among food handlers in hotels and restaurants in Kigali, Rwanda.

Methods: Stool, urine and blood samples from a total of 683 food handlers from 8 different hotels and restaurants in Kigali were collected between 2009 and 2011. Stool specimens were examined microscopically for intestinal parasites. Urine sample were examined microscopically and cultured on bacteriological media. Blood samples were tested for HBsAg and HIV by ELISA.

Results: Of the total subjects examined, 76 (11.2%) were found to be infected by an intestinal parasite. Most frequently found organisms were *Entamoeba histolytica*, *E. coli* and *Giardia sp*. In urine, 140 (20.5%) showed signs of urinary tract infections and the most prevalent bacteria identified were *Escherichia coli* and *Enterococcus sp*. Prevalence of HBV and HIV among food handlers was 5.7% and 3.4% respectively.

Conclusion: The findings from this study indicate that food handlers can be implicated in the spread and transmission of food communicable diseases and reveal the need for protective measures.

http://dx.doi.org/10.1016/j.ijid.2012.05.473

Final Abstract Number: 54.012
Session: Infection Control, Nosocomial Infections & Critical Care
Date: Saturday, June 16, 2012
Time: 12:45-14:15
Room: Poster & Exhibition Area

International epidemic clones of *Acinetobacter baumannii* in Russia

A. Goncharov[1,*], A. Solomennyi[2], T. Suborova[3]

[1] *I.I. Mechnikov North-Western State Medical University, Saint-Petersburg, Russian Federation*
[2] *Institute of Ecology and Genetics of Microorganisms, Perm, Russian Federation*
[3] *S. M. Kirov Military Medical Academy, Saint-Petersburg, Russian Federation*

Background: *Acinetobacter baumannii* is the prevailing pathogen infected the patients admitted to the specialized hospital wards (neurosurgery, traumatology and orthopedics, burns) and intensive care units (ICUs). Nosocomial outbreaks were caused worldwide by clusters of highly similar A.baumannii strains that were assigned by several genotypic methods to three main international clonal lineages named as international clones I, II and III.

There is no enough data about the epidemic clonal types prevailing in Russian hospitals.

Methods: A total of 63 outbreak-related strains of Acinetobacter baumannii isolated between 2004 and 2011 at the 4 ICUs in St. Petersburg (Northwest of Russia), at the burn hospital in Chelyabinsk and surgical ICU in Perm (Ural region) were characterized with respect to clonal relationships by using VNTR typing (MLVA) according to published recently protocol presented by Pourcel et al. [2011]. Nearly all the strains were representative of cross-transmission episodes, and were isolated with identical RAPD typing patterns from more than two patients of the same or different institutions. Thus, the studied strains were classified to 11 RAPD - types. The distribution of RTX - type toxin gene, located in the genomic island pA18 [Iacono M, Villa L, Fortini D, 2008] has been monitored by PCR analyses.

Results: It was found based on MLVA profiles clustering all strains were closely related to international clones I, II and III. The clonal line II was most prevalent (5 from 11 RAPD types). Strains of this clonal lineage were associated with two large outbreaks in pediatric and oncology hospitals in St. Petersburg. RTX- toxin gene was detected only in isolates of this clone.

Conclusion: It seems the international epidemic clones are disseminated in a large geographical area of European Russia and the Urals. Potentially mobile RTX-toxin gene was found in the Russian international clone II strains, as well as in the related European strains (such as ACICU). These data suggest a common epidemiological area which includes Western and Eastern Europe to the Urals.

http://dx.doi.org/10.1016/j.ijid.2012.05.474